**In the Specification:**

Please amend the specification as shown:

Please delete the paragraph on page 3, lines 18-21 and replace it with the following paragraph:

The first strand may contain a sequence selected from the group consisting of AACCTTTGGAGAAGATACTGT **(SEQ ID NO: 1)**, AATCACATTTGAGCTTGATGA **(SEQ ID NO: 2)**, AAGTTGCTGGTTTTGCAAAGT **(SEQ ID NO: 3)**, AAGGATGAGGAAGGCAATTTA **(SEQ ID NO: 4)**, AAGCTCCTAATTACACTCAAC **(SEQ ID NO: 5)**, and AATGTTACAGGGTTTCATACT **(SEQ ID NO: 6)**.

Please delete the paragraph on page 3, line 22 to page 4, line 7 and replace it with the following paragraph:

the invention also provides a method of detecting a SARS virus in a sample, by (a) contacting RNA obtained from the sample with a gene specific primer containing a 3' region that is complementary to a SARS sequence and a 5' sequence that is not complementary to a SARS sequence and synthesizing a first strand cDNA molecule by reverse transcription followed by (b) amplifying the first strand cDNA in a PCR using a pair of primers, where the first primer is complementary to the 5' region of the gene specific primer and where the second primer contains a sequence in the SARS genome that is upstream of the region recognized by the 3' region of the gene specific primer, and (c) detecting the product of the PCR. The gene specific primer may be complementary to a SARS npsl, nps9 or spike sequence, for example. The gene specific primer may contain a sequence selected from the group consisting of GAA CAT CGA TGA CAA GCT TAG GTA TCG ATA gac aac ctg ctc ata aa **(SEQ ID NO: 7)**, GAA CAT CGA TGA CAA GCT TAG GTA TCG ATA gag gat ggg cat cag ca **(SEQ ID NO: 8)**, and GAA CAT CGA TGA CAA GCT TAG GTA TCG ATA gtg tta aaa cca gaa gg **(SEQ ID NO: 9)**. The first primer may contain the sequence GAACATCGATGACAAGCTTAGGTATCGATA **(SEQ ID NO: 10)**. The second primer may contain a sequence selected from the group consisting of GGG AAG TTC AAG GTT ACA AGA ATG TGA GAA **(SEQ ID NO: 11)**, CGG TGT AAG TGC AGC CCG TCT TAC ACC

GTG **(SEQ ID NO: 12)**, and CCT TGA CCG GTG CAC CAC TTT TGA TGA TGT **(SEQ ID NO: 13)**.

Please delete the paragraph on page 4, lines 8-26 and replace it with the following paragraph:

The invention further provides a method of treating or preventing a coronavirus infection in a subject, such as a SARS virus infection, by administering to the subject an effective amount of a composition containing an isolated double stranded RNA molecule, where the RNA molecule contains a first strand containing a ribonucleotide sequence which corresponds to a nucleotide sequence of a coronavirus and a second strand containing a ribonucleotide sequence which is complementary to the nucleotide sequence of the coronavirus, where the double-stranded molecule inhibits expression of the nucleotide sequence of the coronavirus. The first and second strands may be separate complementary strands, or may be contained in a single molecule, where the single molecule contains a loop structure. The nucleotide sequence from the SARS virus may be an nspl sequence, an nsp9 sequence or a spike sequence, for example. The first strand may contain a sequence selected from the group consisting of AACCTTTGGAGAAGATACTGT **(SEQ ID NO: 1)**, AATCACATTTGAGCTTGATGA **(SEQ ID NO: 2)**, AAGTTGCTGGTTTTGCAAAGT **(SEQ ID NO: 3)**, AAGGATGAGGAAGGCAATTTA **(SEQ ID NO: 4)**, AAGCTCCTAATTACACTCAAC **(SEQ ID NO: 5)**, and AATGTTACAGGGTTTCATACT **(SEQ ID NO: 6)**. The double stranded RNA molecule may contain a sequence selected from the group consisting of SC2, SC5, SC14 and SC15.

Please delete the paragraph on page 6, lines 3-10 and replace it with the following paragraph:

Figure 3 shows the location of siRNA targets on different SARS coronavirus isolates Target sequences **(SEQ ID NOS 1-6, respectively, in order of appearance)** as designed based upon SARS coronavirus CUHK-WI were used to find it's specificity for different SARS coronavirus isolates. The "mis-match" of the fifth and sixth target sequences (Spike-1 & 2) with GZ-01 isolate was simply because the imcomplete suquence data of GZ01 isolate as submitted; and the mis-match of the third target sequence (nsp9-A) on HKU39849 was

because there is one base pair missing in HKU39849 sequence at position 13496 nt, which was not found in genomic sequence of other isolates.

Please delete the paragraph on page 7, lines 12-13 and replace it with the following paragraph:

Figure 9 shows the 48 siRNA molecules used for cell culture transfection to test their anti-SARS-CoV activities **(SEQ ID NOS 18, 5, 2, 6, 4, 1, 19-60, respectively, in order of appearance)**.

Please delete the paragraph on page 14, lines 16-34 and replace it with the following paragraph:

The released virus in the culture medium was determined by titration of viral yield in the culture supernatant using CPE-based TCID50 test. The culture supernatant was serially diluted at 10 fold with MEM and inoculated to the FRhK- 4 cells in 96 well plate. The results were evaluated after 3 days of culture. Intracellular copy numbers of viral genome RNA were quantified using a real- time quantitative RT-PCR (Q-RT-PCR). The cells were washed twice with PBS, and total RNA was extracted from the cells using a QIAamp RNA Isolation Kit (Roche Molecular Biochemicals). First strand cDNA was synthesized using RNA H+ Reverse Transcriptase (Invitrogen) and random primers. Two micro liters of reverse transcription products from each reaction was used for PCR. The forward primer (5'-GCATGAAATTGCCTGGTTCAC-3 ' **(SEQ ID NO: 14)**, at a final concentration of 900 nM), reverse primer (5'-GCATTCCCCTTTGAAAGTGTC-3' **(SEQ ID NO: 15)**, at a final concentration of 900 nM) and fluorescence probe (FAMAGCTACGAGCACCAGACACCCTTCGAAA-TRMA **(SEQ ID NO: 16)**, at a final concentration 250 nM) were mixed with Master Mix and subjected to real-time PCR using ABI7900 Sequence Detection System (ABI, Foster City, CA, USA).

The conditions for running PCR were: 50°C for 5 minutes, 95°C for 10 minutes and 40 cycles of 95°C for 15 seconds and 61°C for 1 minute. All measurements were conducted 3 times for statistical analysis.

Please delete the table on page 22, lines 1-2 and replace it with the following table:

| *Genes* | Targeted sequences (5'-3') | | *Locations* |
|---|---|---|---|
| nspl | 1 | AACCTTTGGAGAAGATACTGT **(SEQ ID NO: 1)** | 2711-2731 nt |
| | 2 | AATCACATTTGAGCTTGATGA **(SEQ ID NO: 2)** | 2762-2782 nt |
| nsp9 | 1 | AAGTTGCTGGTTTTGCAAAGT **(SEQ ID NO: 3)** | 13467-13487 nt |
| | 2 | AAGGATGAGGAAGGCAATTTA **(SEQ ID NO: 4)** | 13520-13540 nt |
| S (spike) | 1 | AAGCTCCTAATTACACTCAAC **(SEQ ID NO: 5)** | 21543-21563 nt |
| | 2 | AATGTTACAGGGTTTCATACT **(SEQ ID NO: 6)** | 21659-21679 nt |

Please delete the paragraph on page 23, lines 6-8 replace it with the following paragraph:

Primer 1: Forward-nsplUp (30-mer, 41-70 nt of the putative nspl gene coding sequence, or 2734-2763 nt of coronavirus sequence, AY278554,) 5'---GGG AAG TTC AAG GTT ACA AGA ATG TGA GAA---3' **(SEQ ID NO: 11)**

Please delete the paragraph on page 23, lines 9-12 and replace it with the following paragraph:

Primer 2: SRT-nsplDn (47-mer, the 17-mer at 3' is complementary to 1041-1025 nt of the putative nspl gene coding sequence, or 3734-3718 nt of coronavirus sequence, AY278554). 5'---GAA CAT CGA TGA CAA GCT TAG GTA TCG ATA gac aac ctg ctc ata aa---3' **(SEQ ID NO: 7)**

Please delete the paragraph on page 23, lines 13-15 and replace it with the following paragraph:

Primer3: Forward-nsp9Up (30-mer, 35-64 nt of the putative nsp9 gene coding sequence, or 13381-13410 nt of coronavirus sequence, AY278554). 5'--- CGG TGT AAG TGC AGC CCG TCT TAC ACC GTG---3' **(SEQ ID NO: 12)**

Please delete the paragraph on page 23, lines 16-19 and replace it with the following paragraph:

Primer4: SRT-nsp9Dn (47-mer, the 17-mer at 3' is complementary to 734-718 nt of the putative nsp9 gene coding sequence, or 14080-14064 nt of coronavirus sequence, AY278554). 5'---GAA CAT CGA TGA CAA GCT TAG GTA TCG ATA gag gat ggg cat cag ca---3' **(SEQ ID NO: 8)**

Please delete the paragraph on page 23, lines 20-22 and replace it with the following paragraph:

Primer5: Forward-SpikeUp (30-mer, 45-74 nt of coding sequence of the putative Spike gene coding sequence, or 21511-21540 nt of coronavirus sequence, AY278554). 5'---CCT TGA CCG GTG CAC CAC TTT TGA TGA TGT---3' **(SEQ ID NO: 13)**

Please delete the paragraph on page 23, lines 23-26 and replace it with the following paragraph:

Primer6: SRT-SpikeDn (47-mer, the 17-mer at 3' is complementary to 644-628 nt of the putative Spike gene coding sequence, or 22110-22094 nt of coronavirus sequence, AY278554). 5'---GAA CAT CGA TGA CAA GCT TAG GTA TCG ATA gtg tta aaa cca gaa gg---3' **(SEQ ID NO: 9)**

Please delete the paragraph on page 23, lines 27-28 and replace it with the following paragraph:

Primer 7: (Rev-primer)
5'-AACATCGATGACAAGCTTAGGTATCGATA-3' **(SEQ ID NO: 17)**

**In the Claims:**

Please amend the claims as shown: